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Viral Zoonoses That Fly with Bats: A Review

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Abstract

Emerging infectious diseases are a growing threat to human health and a great challenge for global medical attention systems. Governmental agencies in tropical regions with abundant zoonotic pathogens should implement an active vigilance/monitoring model in bat reservoir populations because of their species richness, abundance and dispersal capabilities. Chiropterans represent approximately 20% of all mammal species, the second largest order in terms of number of species after rodents. Importantly, bats constitute natural reservoirs for potential infection of humans of several infectious disease agents such as *Coronavirus*, *Filovirus*, *Lyssavirus*, *Paramyxovirus*, and *Flavivirus*. Local disease outbreaks caused by new pathogens can expand globally as a result of human intrusion on wildlife ecosystems and subsequent dispersion of pathogens facilitated by international travel—for example, what happened in 2003 during the severe acute respiratory syndrome pandemic (SARS). At this time, it is not possible to predict which pathogen will cross the species barrier in the future. Nonetheless, a better understanding of a holistic transmission process could help the design of strategies to prevent and control of future pandemics. In this work, we present a summary of the potential societal (economic and epidemiological) effect of disease outbreaks of virus families associated with bats, and the preventive and control measures that could be anticipated.

Keywords: tropical medicine, chiropterans, public health, viral diseases

Introduction

Zoonoses are infectious diseases transmitted from free-living or wild animals to humans by direct contact, ingestion, inhalation, or inoculation of infectious material (Dabanch, 2003). The zoonotic etiology includes infectious agents such as viruses, bacteria, parasites, fungi (Dabanch, 2003; Cabello and Cabello, 2008), and prions (Peralta, 2011; Lee et al., 2013). The existence of a sylvatic reservoir species may facilitate the establishment of a zoonosis in a specific area (Collinge and Ray, 2006; Nelson and Holmes, 2007). Generally, wild or sylvatic reservoir animals are asymptomatic, and the zoonotic disease may infect humans via the action of an arthropod vector or the direct transmission from wild or domestic animals (Cabello and Cabello, 2008; Nelson and Holmes, 2007). This paper summarizes what is known of the potential impact that disease outbreaks of bat-associated viruses may have on public health and the economy, and discusses preventive measures that can be implemented to ameliorate them.

Factors that favor the appearance of zoonoses

Multiple causes have been suggested to explain the expansion on zoonotic diseases; in principle they start from three

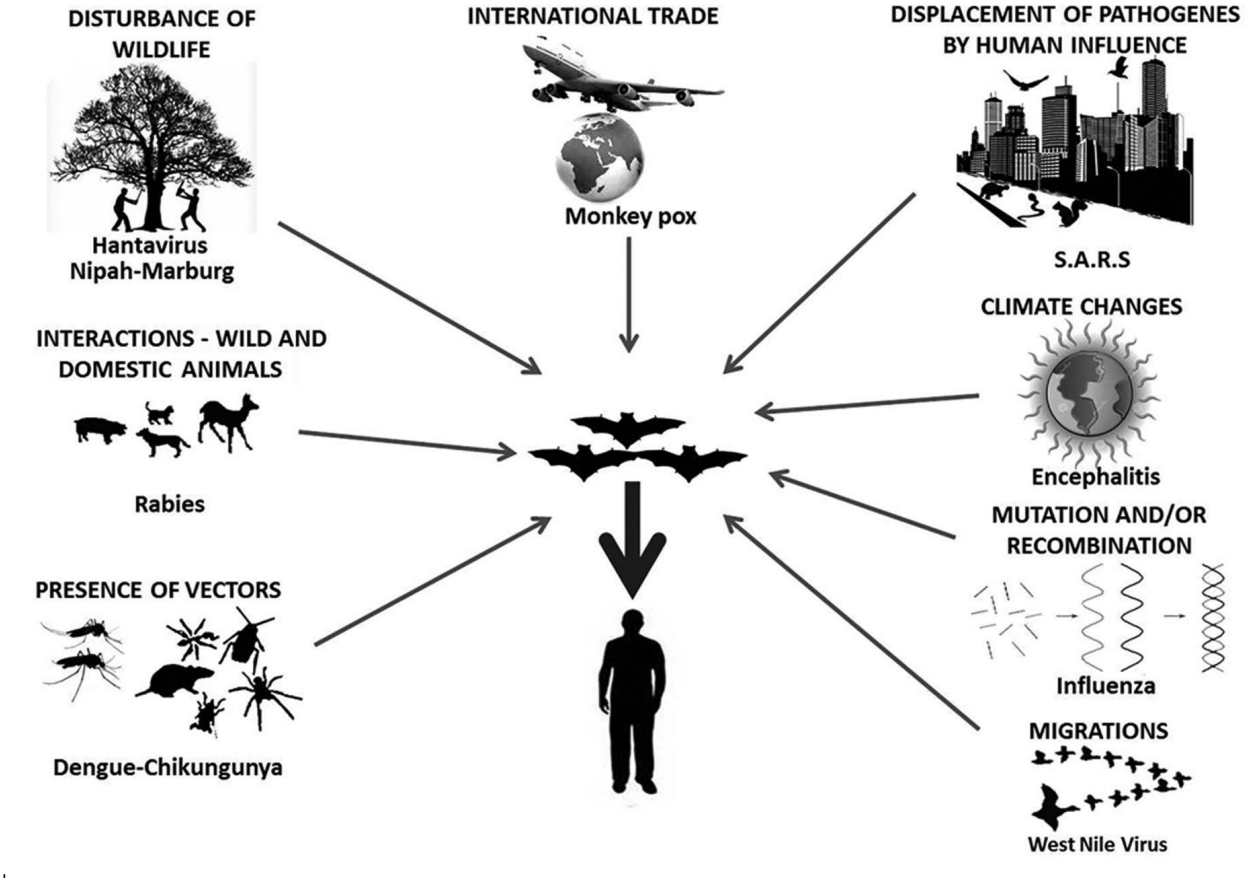

Figure 1. Viral zoonoses that fly.

types of the interactions: a) at the human-animal interface, b) at animal-environment interface, and lastly at c) the human-environment interface: Among a number of specific activities that promote the increase in zoonotic diseases are (Figure 1): habitat modifications that alter the equilibrium in wildlife populations, promote demographic increase in wild reservoirs, and increase the type and number of interactions between humans and animals both wild and domestic (Krause, 1992; Jones et al., 2008); Climate change that causes alterations in the behavior/function of hosts and vectors and that may produce a reduction in the ability to mount an effective immune response (Monsalve et al., 2009) in either, host or vector, or both; Introduction of vectors such as arthropods that mobilize the infection easily in humans—for example, trypanosomiasis, rickettesial infections, *Leishmania*, *Ehrlichia*, Chikungunya, zika, dengue, and various forms of encephalitis, all transmitted by insects or acarines (Bender and Shulman, 2004; Parrish et al., 2008; Collinge and Ray, 2006; Daszak et al., 2001; Bengis et al. 2004).

Bats and their importance as zoonotic reservoirs

Chiropterans (bats) are the only truly flying mammals; with over 1,200 species, they represent no less than 20% of all mammal species and are the second most numerically diverse mammalian order (Ballesteros and Racero, 2012). The number of zoonotic viruses is greater within rodents in comparison with bats, however, on a species-by-species basis bats harbor more viruses (zoonotic and non-zoonotic) than rodents (Luis et al., 2013). There have been more than 60 virus species described from bats, grouped in the following families and genera: *Rhabdoviridae—Lyssavirus*; *Paramyxoviridae—Henipavirus* and *Rubulavirus*; *Flaviviridae—Flavivirus*; *Togaviridae—Alphavirus*; *Bunyaviridae—Orthobunyavirus*, *Phlebovirus*, and *Hantavirus*; *Reoviridae—Orbivirus* and *Orthoreovirus*; and some viruses that have not yet been classified in *Rhabdoviridae* and *Herpesviridae* (Calisher et al., 2006).

Most bat classifications recognize two major groups: Microchiroptera and Megachiroptera. Although it is likely that these groups are not monophyletic (Teeling et al., 2005), this subdivision is useful for didactic purposes. The

suborder Microchiroptera includes the largest diversity of trophic guilds with many species primarily insectivorous but important numbers of species on other trophic categories, including: piscivores, nectarivorous, frugivores, sanguivores, insectivorous, etc. Megachiroptera comprises species classified into only one family (the Pteropodidae, the flying foxes) and includes species whose feeding habits include plant material—either fruit, nectar, or pollen (Kunz et al., 2011; Moratelli and Calisher, 2015).

Bats and their potential for pathogen dispersion

The ability of bats to disperse pathogens may be attributed to several different mechanisms: The need to fly great distances in search for food, a long lifespan (up to 35 years), a gregarious behavior that induces the formation of extended local communities with different species inhabiting the same ecological roosting niche, and –in some cases- large and densely populated roosts. For example, the free-tailed bat, *Tadarida brasiliensis* may roost with up to one million individuals in a single sleeping site [Constantine 1967; Betke et al. 2008]). In a recent review, the sympatric nature of several species roosting in the same cave or cave-system was identified as an important issue in the potential transmission of pathogens among members of different species of bats (Luis et al., 2013).

The capacity of bats to spread pathogens can also be related to a variety of immunological scenarios; by species that hibernate diminish their metabolic rate during hibernation and therefore may reduce their ability to mount an effective immune response. If this scenario is correct, hibernation may facilitate the multiplication of psychrophilic /enteropathogenic bacteria provoking systemic illness in hibernating species, which in turn may amplify the infectious cycle and infectivity. This scenario was proposed for *Yersinia* (Mühldorfer, 2013; Blackwood et al., 2013). The noted characteristics have piqued the interest of investigators who are enthusiastically studying the establishment of the zoonotic potential of bats and their relation to public health (Figure 2).

In what follows, we supply an overview on the main viral pathogens isolated from bats that have the potential to cause disease in humans.

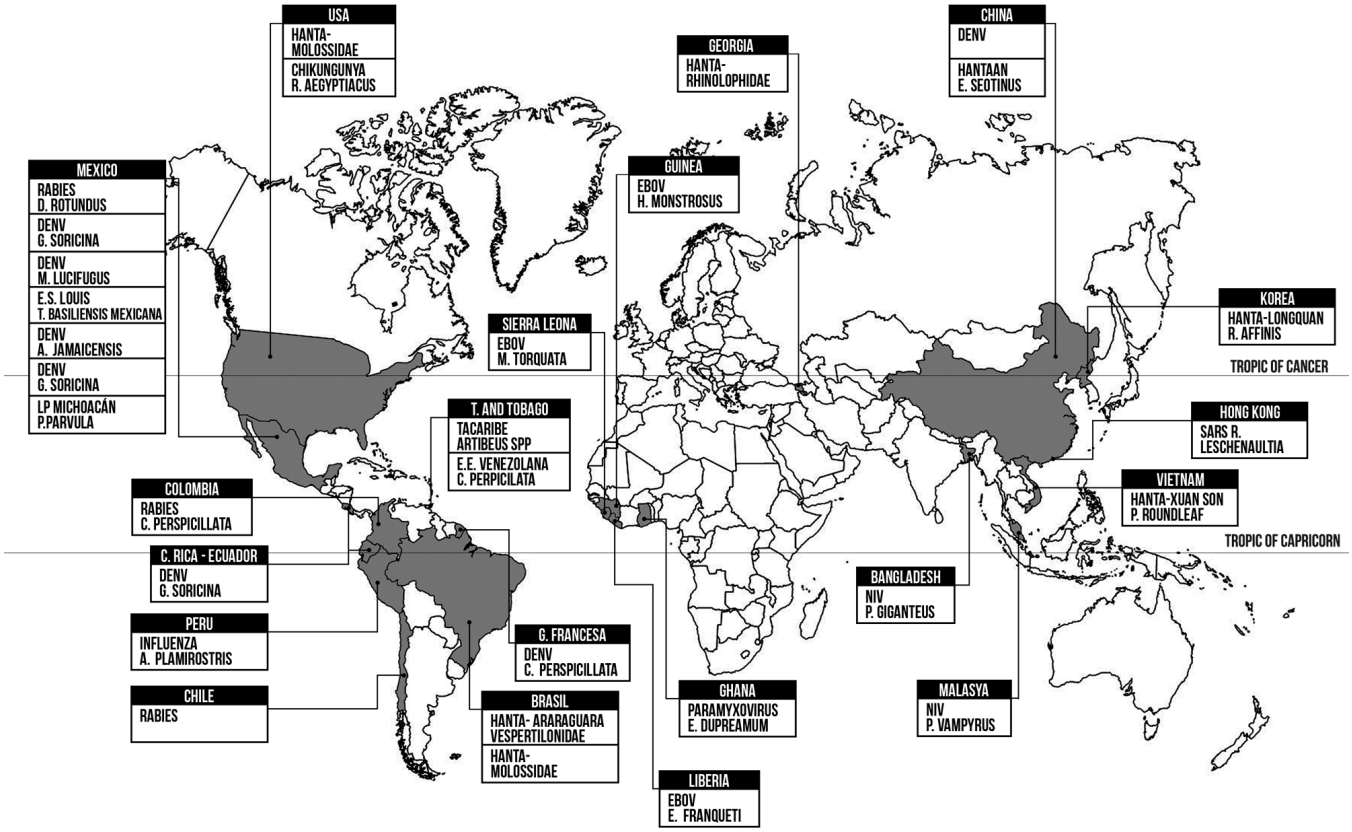

Figure 2. Distribution of some viruses isolated from bats. Please see text for more details.

Viruses

Rabies virus

Without a doubt, this is one of the most infamous viruses transmitted by bats. It is estimated that rabies inflicts over US$30 million in costs associated with livestock mortality alone (WHO, 2013).

Both sanguivore and insectivore bat species are known to serve as reservoirs for rabies virus. Only three species of bats are sanguivores: *Desmodus rotundus* (É. Geoffroy, 1810), *Diaemus youngi* (Jentink, 1893), and *Diphylla ecaudata* Spix, 1823, all occurring in the Neotropics (Bogich et al., 2012; Carvalho et al., 2012). Small, but significant, differences exist in their feeding habits, with *D. rotundus* preferring big mammals, while *D. youngi* and *D. ecaudata* usually less numerically dense and therefore less common, tending to prefer bird blood; non-sanguivorous bats are also reservoirs for rabies and maintain independent endemic cycles. In America they have been reported in Brazil (Uieda et al., 1995; De Araújo et al. 2014), Mexico (Loza et al., 2000), Chile (Favi et al., 2002), and Colombia (Núñez et al., 2001). In Colombia the rabies viruses were isolated from *Carollia perspicillata* (Linnaeus, 1758) (Núñez et al., 2001) and *Eptesicus brasiliensis* (Desmarest, 1819) (Paéz et al., 2003); also group III rabies viruses have been detected in insectivorous bats such as *Molossus*, three domestic dogs and one human (Paéz et al., 2003). Since 2000, vampire bats have been the leading cause of human rabies in Latin America and the Caribbean. A continent-wide report suggests that from 2010 to 2012 there was an increase of 5.2% in bat-transmitted human rabies (Vigilato et al., 2013) and that the effect of the virus appears to be increasing as the virus is emerging in historically Rabies-free areas throughout Latin America (Benavides et al., 2016).

In Colombia two types of transmission cycles have been identified: (1) an urban cycle that circulates primarily among susceptible dogs (dog to dog) but can involve foxes, bovines, horses, and humans, and (2) and a sylvatic cycle, in which sanguivorous (and other) bats are the main reservoirs, but that also may involve bovines, equines, cats, and humans. From the first isolation case of rabies from bats conducted in Colombia (Morales et al., 1968), the country continues to be considered endemic because of the presence of rabies cases linked to bats (Brito et al., 2013; Sarmiento et al. 2015). In northern Brazil, a 2004 outbreak of human rabies was reported (resulting in 20 deaths) that was linked to transmission by *Desmodus rotundus* (Gupta, 2005).

Hantavirus

The Hantaan virus was first described in 1978 (Lee et al., 1978). Hantaviruses have been reported on all continents except Australia and may cause illness with high lethality rates: the hantavirus cardiopulmonary syndrome (SCPH) in the Americas and the hemorrhagic fever with renal syndrome (FHSR) in Asia and Europe (Jonsson et al., 2010; Detlev et al., 2015). The reservoirs initially described correspond to small mammals in the order Rodentia (rodents) and Soricomorpha (shrews); these reservoirs either do not get sick, or if so, they quickly recover (Schonrich et al., 2008; Luis et al., 2013; Detlev et al., 2015). Molecular and serological evidence shows that species of bats from several genera (*Eptesicus*, *Rhinolophus*, *Artibeus*, *Carollia*, *Chiroderma*, *Chrotopterus*, *Desmodus* and *Glossophaga*) tested positive for hantavirus antibodies and, at least some, may act as reservoirs (Kim et al., 1994; Jung et al., 1995; Sabino-Santos et al. 2015). Although there is no hard evidence of transmission of hantavirus from bats to humans (Root et al., 2004; Hinson et al., 2004; Bagamian et al., 2012), hantavirus transmission from human to human was reported for Andes virus (ANDV) (Wells et al., 1997; Martínez et al., 2005), and thus the aerosol transmission from bats to humans is not out of the realm of possibilities..

Cases of Hantavirus Pulmonary Syndrome have been diagnosed in Argentina, Brazil, Paraguay, Bolivia, Chile, Uruguay, Panama, and, recently, in Peru, where numerous viral genotypes have been identified from both humans and rodents (Jonsson et al., 2010; Luiz et al., 2014). In Colombia, in 2004 and 2006 the first serologic studies performed in the Colombian Caribbean were published showing the circulation of hantavirus in humans (Máttar et al., 2004) and in rodents (Alemán et al., 2006) using antigens from the "virus sin nombre" (SNV). Afterwards, in 2011, the genetic identification of a new hantavirus was made in rodents from the Uraba in Colombia (Londoño et al., 2011). In 2012, another study showed the infection in humans with hantavirus antigens from South American strains Maciel and Araraquara (Guzmán et al., 2012), and in 2014 we had the first clinical case in humans (Máttar et al., 2014).

Mammarenavirus

The mammarenaviruses have a bi-segmented RNA genome consisting of a simple chain and negative sense. The mammarenaviruses are phylogenetically divided into two broad groups: old world and new world. Normally these viruses use rodents as reservoirs, however, Tacaribe (TCRV) is unusual in this respect. This virus occurs in bats and was first isolated from *Artibeus jamaicensis palmarum* Leach, 1821 and *Artibeus jamaicensis trinitatis* during a survey of virus surveillance of rabies in Trinidad between 1956 and 1958 (Salazar-Bravo, Ruedas and Yates 2002). Mammarenavirus infect and cause human disease in many parts of the world

(Charrel et al., 2010). Tacaribe mammarenavirus is, apparently, non-pathogenic to humans and for this reason has proved to be an excellent study model that can be studied without the need for BSL-4 facilities (Martínez et al., 2009). Recently the Tacaribe virus was isolated from the tick *Amblyoma americanum* Linnaeus, 1758 collected in Florida (Sayler et al., 2014).

Paramyxoviridae

Two species of Henipavirus (*Hendra* and *Nipa*) and two of Rubulavirus (*Tioman* and *Menangle*) (Mononegavirales: Paramyxoviridae) were identified as causative agents of independent disease outbreaks in Australasia; symptoms included acute encephalitis, or as an acute influenza-like illness leading to severe respiratory distress, or as meningitis (Marsh et al., 2012; Chua et al., 2001).

Hendra virus, discovered in 1994, was identified in a respiratory disease outbreak that infected 20 horses and two humans, killing all the horses and one of the humans (Smith and Wang, 2013). It has re-appeared several times since the original outbreak (Murray et al., 1995; Marsh et al., 2012). In humans the mortality rate of the infection is 57%. Species of bats in the genus *Pteropus* are the natural reservoirs and do not show clinical symptoms, even after experimental infection (Williamson et al., 1998; Halpin et al., 2011; Middleton et al., 2007; Field et al., 2001). It has been suggested that the geographic extent of these viruses is limited by the distribution of its host species, as they include Australia, Asia, and islands off East Africa but not continental Africa. Therefore, it was believed that the distribution of henipaviruses could be geographically restricted, until serological and molecular work showed the presence of henipavirus in *Eidolon helvum* (Kerr, 1792) from Ghana, West Africa, and in *Eidolon dupreanum* (Pollen in Schlegel and Pollen, 1866) from Madagascar (Hayman et al., 2008; Drexler et al., 2009). Currently, various paramyxoviruses have been described from bats from most continents (Lau et al., 2010; Kurth et al., 2012; Wilkinson et al., 2012; Baker et al., 2012), but the pathogenic potential of these virus in humans is still unknown. A serologic study conducted in Mexico detected a paramyxovirus from the genus *Rubulavirus* named "La Piedad de Michoacán" virus (LPM) that affected juvenile pigs, *Sus scrofa* Linnaeus, 1758, producing encephalitis, infertility, and opacity in the cornea (blue eye disease); the precise origin of LPM was not established (Salas et al., 2004); diseases caused by paramyxovirus in other countries have not been reported.

Two major outbreaks of the Nipah virus have taken place since the mid-1990s, one in Malaysia and Singapore and one in Bangladesh and India. The outbreak in Malaysia (September 1998–June 1999) caused respiratory and neurologic illness in pigs. Transmission from pigs to humans produced 283 cases and 109 deaths (39% lethality). In Singapore 11 cases were reported, with the death of one slaughterhouse worker. The outbreak was controlled by killing more than 1.1 million pigs from the areas at-risk (Paton et al., 1999). The NiV reservoirs in Malaysia are *Pteropus vampyrus* (Linnaeus, 1758) and *Pteropus hypomelanus* Temminck, 1853 (see summary in Yob et al., 2001), and in the case of Bangladesh and India the host species is *P. giganteus* (Brünnich, 1782) (see summaries in Smith and Wang, 2013; Yadav et al., 2012).

Filovirus

Ebola and Marburg viruses are the only known members of the family *Filoviridae*; they cause hemorrhagic viral fever (FHV) in humans, greater apes, and other mammals with lethality percentages ranging from 53% to 90% (Leroy et al., 2011). The filovirus from the genus *Marburgvirus* (MARV) comprises only one species, while five strains have been described for Ebola (EBOV) (Kuhn et al., 2010; Barrette et al., 2009). The virus was first detected in 1976 when two simultaneous outbreaks occurred in Nzara (Sudan) and Yambuku (Democratic Republic of the Congo). Fruit-eating bats, in particular *Hypsignathus monstrosus* Allen, 1861; *Epomops franqueti* (Tomes, 1860); and *Myonycteris torquata* (Dobson, 1878), have been suggested as possible natural hosts of the Ebola virus in Africa. The geographic distribution of EBOV may coincide with the distribution of these African bats (Feldmann et al., 2011, 2014). The most recent outbreak of Ebola virus started in December 2013 in southeastern Guinea (West Africa) subsequently spreading to Liberia, Sierra Leone, and other countries, to become the most long-term and most widespread geographically since the discovery of the Ebola virus (de La Vega et al., 2015). At the end of the epidemic over 28, 000 suspected, probable and confirmed cases of Ebola virus disease (EVD) were reported, although the true toll of the epidemic, especially the number of deaths, was probably greater. A total of 11,310 deaths was recorded, but the true toll was certainly greater (WHO 2016).

Ebola is spread in the human population from close contact with organs, blood, secretions, or other bodily fluids from animal and human corpses that are infected. In Africa, documented cases of infection are associated with the manipulation of chimps, gorillas, fruit bats, monkeys, antelope, and porcupines that were infected, sick, or dead in the jungle (Olival et al., 2014). Ancestral traditions of contact with the deceased may also be a cause of transmission. Men can transmit the virus through semen even seven weeks after clinical recuperation. Infections of health care personnel happen when treating patients

with EBOV without having taken the necessary preventive measures in the use of required biosafety equipment (WHO, 2014).

Coronavirus

Coronaviruses (CoV) are members of the subfamily *Coronavirinae*, and together with the *Torovirinae* they form the family *Coronaviridae* (see King et al., 2012). In 2003 a global outbreak of SARS that started in eastern China and Hong Kong caused 8,422 cases and 916 human deaths (10.9% lethality) around the world (WHO, 2003). It was believed that the virus went through a quick process of adaptation in an intermediate host (the palm civet, *Paguma* sp.) before transmission to humans was possible; the fruit bat *Rousettus leschenaultia* was identified as the reservoir of coronavirus SARS (Li et al., 2005). The outbreak of SARS-CoV was estimated to cost $54 million dollars worldwide (Kimball et al., 2004). Coronavirus was detected from bats in Mexico (Machain et al., 2013).

Flavivirus

The flavivirus (FV) are the cause of important diseases such as dengue, yellow fever, West Nile virus, and San Luis encephalitis virus. Specimens belonging to 5 families, 12 genera, and 19 species of different bats were checked for the dengue virus using ELISA and RT-PCR tests in endemic areas of the Pacific and the Gulf of Mexico, with seropositive results in nine individuals from four different species: the insectivores *Myotis nigricans* (4/12), *Pteronotus parnellii* (3/19), and *Natalus stramineus* (1/4), and one frugivore, *Artibeus jamaicensis* (1/35). Through RT-PCR, serotype 2 of the dengue virus was detected in 4 samples of 3 species (all from the Gulf coast during the rainy season): two fruit-eating bats, *A. jamaicensis* (2/9) and *Carollia brevicauda* (1/2), and one insectivore *M. nigricans* (1/11). This last one tested positive simultaneously by serology and molecular biology (Aguilar et al., 2008). In Yucatan (Mexico) during 2010, 140 bats were captured from 7 species. The bats with positive antibodies to the virus belonged to 3 species: the nectarivore *Glossophaga soricina* and two fruit bats, *Artibeus jamaicensis* and *Artibeus lituratus*; flavivirus prevalence was 33%, 24%, and 9%, respectively. Each sample of the serum was tested to determine the presence of flavivirus through reverse transcription PCR (RT-PCR), but all samples were negative (Quan et al., 2013). A viral diversity study in bats from Guatemala, Cameroon, Nigeria, Democratic Republic of the Congo, Kenya, and Mexico detected hepacivirus and pegiviruses, a genus recently designated within the family *Flaviviridae*, and related to the hepatitis virus in humans (Luis et al., 2013; Zhang et al., 1998). The dengue virus was also detected using RT-PCR in bats captured in Hayman, China (Platt et al., 2001). In Ecuador, there are reports of dengue antibodies in bats (Tong et al., 2013).

Influenza virus

A new subtype of the influenza virus (H17N10) was discovered in fruit-eating bats in Central America, suggesting that other species may transport divergent variants of the influenza virus. In Peru, and via RT-PCR, a new influenza A virus was identified in *Artibeus planirostris* (Spix, 1823) fruit bats and denoted as (H18N11) (Banyard et al., 2014). (Table 1).

Public Health Measures

Public health strategies to combat human infection from bat-borne (and other) zoonotic viruses should take into account the ecological and social context of their region. Nonetheless, an understanding of bat ecology and their viral pathogens, as well as the identification of factors that may facilitate an outbreak, could facilitate the control and the reduction of emergent zoonosis. By understanding the triggering mechanisms of an outbreak, management plans and risk mitigation processes can be developed. Once identified, the strategies for risk reduction may be implemented through education of the general public and doctors, veterinarians, and politicians (Smith et al., 2011). According to the ecosocial context, some measures could be useful for reducing the risk of transmission, such as the adequate use of protection equipment in the treatment of patients or animals and restrictions on the commercialization and consumption of wild meat (in countries that consume bat meat). As a result of past outbreaks, public health measures implemented have included improved vigilance and increased infection control for hospitals in the case of SARS, CoV, EBOV, and NIV, and during veterinary procedures in the case of Hendra virus, where the use of quarantine and the localization of contacts have been implemented to limit the propagation of the virus (Smith and Wang, 2013). The importance of implementing strategic communication has also been suggested for informing the public with the objective of avoiding the propagation of risk activities (WHO, 2003).

The application of control and prevention measures can be accomplished at different levels. Changes in agricultural practices, such as the creation of dampening barriers between fruit trees and at stables where domestic animals are maintained could significantly reduce the NIV and Hendra virus transmission; this measure has played an important role in the prevention of new NIV outbreaks in

Table 1. Family and genus of viruses isolated from bats

Family/genus	Virus	Host	Food source**	Reference
Rhabdoviridae/ Lyssavirus	Rabia*	*D. rotundus*	Sanguivore	Kim et al. 1994
		E. brasiliensis	Insectívore	Morales et al. 1968
	Lagos bat	*E. helvum*	Frugivore	Tong et al. 2103
		E. dobosonii	Frugivore	Tong et al. 2103
		N. gambiensis	Insectivore	Tong et al. 2103
		E. wahlbergi	Frugivore	Tong et al. 2103
	Duvenhage	*N. noctula*	Insectivore	Tong et al. 2103
		V. murinus	Insectivore	Calisher et al. 2006
		N. thebaica	Insectivore	Calisher et al. 2006
	A. bat lyssavirus	*Pteropus spp*	Frugivore	Calisher et al. 2006
		S flaviventris	Insectivore	Calisher et al. 2006
	E. bat Lyssavirus 1	*E. serotinus*	Insectivore	Calisher et al. 2006
		R. aegyptiacus	Frugivore	Calisher et al. 2006
	Aravan	*M. blyhii*	Insectivore	Calisher et al. 2006
	Khujand	*M. mystacinus*	Insectivore	Calisher et al. 2006
	Irkut	*M. leucogaster*	Insectivore	Calisher et al. 2006
	W. Caucasian bat	*M. schreibersii*	Insectivore	Calisher et al. 2006
Bunyaviridae/ Hantavirus	Hantaan	*E. serotinus*	Insectivore	Weiss et al. 2012
		R. ferrumequinum	Insectivore	Weiss et al. 2012
	Magboi	*N. hispida*	Insectivore	Aguilar et al. 2005
	Mouyassue	*N. nanus*	Insectivore	Sumibcay et al. 2012
	Longquan	*R. afinis*	Insectivore	Guo et al. 2013
		R. onoceros	Insectivore	Guo et al. 2013
		R. sinicus	Insectivore	Guo et al. 2013
	Huangpi	*P. abramus*	Insectivore	Guo et al. 2013
	Xuan son	*H. Pomona*	Insectivore	Arai et al. 2013
Togaviridae/ alphavirus	Chikungunya	*Scotophilus sp*	Insectivore	Arai et al. 2013
		R. aegyptiacus	Frugivore	Arai et al. 2013
		H. caffer	Insectivore	Arai et al. 2013
		C. pumilus	Insectivore	Arai et al. 2013
	Sindbis	*Rhinolophidae* sp	Insectivore	Karabatsos, 1985
		Hipposideridae sp	Insectivore	Karabatsos, 1985
	E. E. Venezolana*	*D. rotundus*	Sanguivore	Calisher et al. 2006
		U. bilobatum	Frugivore	Calisher et al. 2006
		A. phaeotis	Frugivore	Calisher et al. 2006
Coronaviridae/ coronavirus	S.A.R.S.	*R. leschenautitia*	Insectivore	Li et al. 2005
		R. sinicus	Insectivore	Li et al. 2005
		R. pearsonii	Insectivore	Li et al. 2005
		R. macrotis	Insectivore	Li et al. 2005
		R. ferrumequinum	Insectivore	Li et al. 2005
Filoviridae/ filovirus	Ébola	*H. monstrosus*	Frugivore	Leroy et al. 2011
		E. franqueti	Frugivore	Leroy et al. 2011
		M. torquata	Frugivore	Leroy et al. 2011

(continued)

Table 1 (continued). Family and genus of viruses isolated from bats

Family/genus	Virus	Host	Food source**	Reference
	Dengue*	*M. nigricams*	Insectivore	Zhang et al. 1998
		P. parnellii	Insectivore	Zhang et al. 1998
		N. stramineus	Insectivore	Zhang et al. 1998
		A. jamaicensis	Frugivore	Zhang et al. 1998
	Bukalasa*	C. pumilus	Insectivore	Downs et al. 1963
		T. condylura	Insectivore	Downs et al. 1963
	Carey I.	*C. brachiotis*	Frugivore	Downs et al. 1963
		M. minimus	Nectarívoro	Downs et al. 1963
	Dakar	*C. pumilus*	Insectivore	Downs et al. 1963
		T. perforates	Insectivore	Downs et al. 1963
		Scotophilus sp	Insectivore	Downs et al. 1963
		M. condylurus	Insectivore	Downs et al. 1963
Flaviridae/	Entebbe	*C. pumilus*	Insectivore	Downs et al. 1963
Flavivirus	E. Japonesa	*H. armiger*	Insectivore	Downs et al. 1963
		M. schreibersii	Insectivore	Downs et al. 1963
		R. cornutus	Insectivore	Downs et al. 1963
	Jugra	*C. brachiotis*	Frugivore	Downs et al. 1963
	Kyasanu forest	*R. rouxi*	Insectivore	Downs et al. 1963
		C. sphinx	Frugivore	Downs et al. 1963
		R. rouxi	Insectivore	Downs et al. 1963
		C. sphinx	Frugivore	Downs et al. 1963
	Río Bravo*	*T. brasiliensis*	Insectivore	Varelas et al. 1982
		E. fuscus	Insectivore	Varelas et al. 1982
	Ponh Penh	*E. spelaea*	Pollen	Downs et al. 1963
		C. brachyotis	Frugivore	Downs et al. 1963
	E. S. Louis*	*T. brasiliensis*	Insectivore	Downs et al. 1963
	Saboya	*N. gambiensis*	Insectivore	Downs et al. 1963
	Sokuluk	*N. gambiensis*	Insectivore	Price, 1978
		V. pipistrellus	Insectivore	Downs et al. 1963
	Tamana	*P. parnellii*	Insectivore	Downs et al. 1963
	Uganda	*Rousettus* sp	Frugivore	Downs et al. 1963
		Tadarida sp.	Insectivore	Downs et al. 1963
	Nipah	*P. pliocephalus*	Pollen	L'vov et al. 2014
		P. scopulatus	Pollen-Fruit	Yob et al. 2001
		P. conspicillatus	Frugivore	Yob et al. 2001
	Hendra	*P. alecto*	Pollen-Fruit	Tajima et al. 2005
Paramyxoviridae/		*P. pliocephalus*	Frugivore	Epstein et al. 2008
Rubulavirus		*P. scopulatus*	Pollen-Fruit	Epstein et al. 2008
		P. conspicillatus	Frugivore	Epstein et al. 2008
	Mapuera	*S. lilium*	Frugivore	Epstein et al. 2008
	Mengale	*P. pliocephalus*	Pollen	Smith et al. 2011
	L P. Michoacán	*P.parvula*	Insectivore	Paton et al. 1999
Arenaviridae/	Tacaribe*	*A. lituratus*	Frugivore	Downs et al. 1963
Arenavirus		*A. jamaicensis*	Frugivore	Downs et al. 1963

***** Viruses isolated from bats in America.

****** Principal food source

Malaysia. The introduction of biologic containment measures on pig farms should include vigilance toward animals transferred from other areas and those sent to the slaughterhouse. This is another effective approach that can be applied with relative ease with respect to farming, livestock, and the commercialization of animals (Smith and Wang, 2013). Another measure could be to implement an active vigilance model on different bat populations for the purpose of detecting potential zoonotic agents as well as unknown viruses of low pathogenicity that could recombine with other viruses to become pathogens (Brown, 2004).

Holistic approaches such as ecological studies and a combination of field and laboratory practices will be of great use in creating predictive models that will allow for a better understanding of bioecological aspects and the generation of management options for disease, regardless of the source or virus. For example, a community could establish management options that would reduce the probability of contact between humans and reservoirs during seasonal periods (high risk of a jump between species); such methods could be effective in balancing the conservation needs of biodiversity and the need for human health policies. Finally, the use of new technologies like serological multiplexing and high-efficiency sequencing are being used as an integral part of the efforts to increase our supervision capacity of pre-emergency pathogens with zoonotic potential.

Conclusion

The widespread geographical distribution of Chiroptera and their viral biodiversity suggests that bats are an important natural reservoir for viruses of growing interest in the transmission of infectious zoonotic diseases with an impact on public health and which also might implicate great economic loses. Knowledge of the distribution of reservoirs and studies on their specific role in the transmission of zoonotic viral agents are necessary to establish risk areas and to contribute to prevention and control.

Public health policies demand a holistic approach that integrates international scientific cooperation. The global Ebola epidemic, for example, showed that it is necessary to conform multidisciplinary teams made up of ecologists, veterinarians, social scientists, and politicians who work together to minimize the impact of zoonotic diseases and at the same time to assume the challenge of coexisting with species that are vital to the ecosystem.

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